

Serial Number: 09/549,096A

CRF Processing Date: 2/26/2002  
 Edited by: [Signature]  
 Verified by: [Signature] (STIC staff)

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: 11044
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



1600

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/549,096A

TIME: 13:30:58

Input Set : A:\pto.amc.txt

Output Set: N:\CRF3\02262002\I549096A.raw

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6 <110> APPLICANT: WARE, CARL F.
8 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND
9   METHODS OF USE
11 <130> FILE REFERENCE: 051501/0276397
13 <140> CURRENT APPLICATION NUMBER: 09/549,096A
14 <141> CURRENT FILING DATE: 2000-04-12
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 29
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
28 <400> SEQUENCE: 1
29 cggagatctg agttcatcct gctagctgg      29
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 31
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
40 <400> SEQUENCE: 2
41 ataggatccc ttggtctggt gctgacattc c  31
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 29
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
52 <400> SEQUENCE: 3
53 gacgtcagat cttcccacct ttcctccta    29
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 29
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
64 <400> SEQUENCE: 4
65 gaacagagat ctcattgctc ctggctctg    29
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 1169
70 <212> TYPE: DNA

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## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/549,096A

TIME: 13:30:58

Input Set : A:\pto.amc.txt

Output Set: N:\CRF3\02262002\I549096A.raw

71 &lt;213&gt; ORGANISM: Homo sapiens

73 &lt;220&gt; FEATURE:

74 &lt;221&gt; NAME/KEY: CDS

75 &lt;222&gt; LOCATION: (49)..(771)

77 &lt;400&gt; SEQUENCE: 5

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78 gaggttgaag gaccagcg tgctcagccct gctccagaga ccttgggc atg gag gag 57
79                                     Met Glu Glu
80                                     1
82 agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc 105
83 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile
84      5              10              15
86 cca ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg 153
87 Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser Cys Ser Val
88 20              25              30              35
90 gcc cgg gtg ggt ctg ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg 201
91 Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly Ala Gly Leu
92              40              45              50
94 gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag 249
95 Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu
96              55              60              65
98 atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg 297
99 Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu
100      70              75              80
102 ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca 345
103 Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr
104      85              90              95
106 ggg gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag 393
107 Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu
108 100              105              110              115
110 act cag ctg ggc ctg gcc tcc ctg agg ggc ctc agc tac cac gat ggg 441
111 Thr Gln Leu Gly Leu Ala Ser Leu Arg Gly Leu Ser Tyr His Asp Gly
112              120              125              130
114 gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg 489
115 Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
116              135              140              145
118 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc 537
119 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
120      150              155              160
122 cac ggc ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg 585
123 His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu
124      165              170              175
126 ttg gtc agc cag cag tca ccc tgc gga cgg gcc acc agc agc tcc cgg 633
127 Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg
128 180              185              190              195
130 gtc tgg tgg gac agc agc ttc ctg ggt ggt gtg gta cac ctg gag gct 681
131 Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His Leu Glu Ala
132              200              205              210
134 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
135 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu

```

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/549,096A

TIME: 13:30:58

Input Set : A:\pto.amc.txt

Output Set: N:\CRF3\02262002\I549096A.raw

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136          215          220          225
138 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga          771
139 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
140          230          235          240
142 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc 831
144 aggggaaaga aaactcacga agcagaggct gggcgtggtg gctctgcct gtaatcccag 891
146 cactttggga ggccaaggca ggcggatcac ctgaggtcag gagttcgaga ccagcctggc 951
148 taacatggca aaaccccatc tctactaaaa atacaaaaaat tagccggacg tgggtggtgcc 1011
150 tgcctgtaat ccagctactc aggaggctga ggcaggataa ttttgcttaa acccgggagg 1071
152 cggaggttgc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
154 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa          1169
157 <210> SEQ ID NO: 6
158 <211> LENGTH: 240
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 6
163 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
164 1          5          10          15
166 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
167          20          25          30
169 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
170          35          40          45
172 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
173          50          55          60
175 Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
176 65          70          75          80
178 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
179          85          90          95
181 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
182          100          105          110
184 Leu Trp Glu Thr Gln Leu Gly Leu Ala Ser Leu Arg Gly Leu Ser Tyr
185          115          120          125
187 His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
188          130          135          140
190 Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
191 145          150          155          160
193 Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
194          165          170          175
196 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
197          180          185          190
199 Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
200          195          200          205
202 Leu Glu Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu
203          210          215          220
205 Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
206 225          230          235          240

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**VERIFICATION SUMMARY**

DATE: 02/26/2002

PATENT APPLICATION: US/09/549,096A

TIME: 13:30:59

Input Set : A:\pto.amc.txt

Output Set: N:\CRF3\02262002\I549096A.raw



1644

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/549,096A

DATE: 02/19/2002

TIME: 12:15:59

Input Set : A:\Sequence Listing.asc

Output Set: N:\CRF3\02192002\I549096A.raw

Does Not Comply  
Corrected Diskette Needed

6 <110> APPLICANT: WARE, CARL F.  
 8 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND  
 9 METHODS OF USE  
 11 <130> FILE REFERENCE: 051501/0276397  
 13 <140> CURRENT APPLICATION NUMBER: 09/549,096A  
 14 <141> CURRENT FILING DATE: 2000-04-12  
 16 <160> NUMBER OF SEQ ID NOS: 6  
 18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 29  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 28 <400> SEQUENCE: 1  
 E--> 29 cggagatctg agttcatcct gctagctgg → 29 (format error)  
 30 29  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 31  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 41 <400> SEQUENCE: 2  
 E--> 42 ataggatccc ttggtctggt gctgacattc c same error  
 43 31  
 46 <210> SEQ ID NO: 3  
 47 <211> LENGTH: 29  
 48 <212> TYPE: DNA  
 49 <213> ORGANISM: Artificial Sequence  
 51 <220> FEATURE:  
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 54 <400> SEQUENCE: 3  
 E--> 55 gacgtcagat cttccacct ttctctcta same  
 56 29  
 59 <210> SEQ ID NO: 4  
 60 <211> LENGTH: 29  
 61 <212> TYPE: DNA  
 62 <213> ORGANISM: Artificial Sequence

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/549,096A

DATE: 02/19/2002

TIME: 12:15:59

Input Set : A:\Sequence Listing.asc

Output Set: N:\CRF3\02192002\I549096A.raw

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64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
67 <400> SEQUENCE: 4
E--> 68 gaacagagat ctcattgctc ctggctctg
69 29
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 1169
74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
77 <220> FEATURE:
78 <221> NAME/KEY: CDS
79 <222> LOCATION: (49)..(771)
81 <400> SEQUENCE: 5
E--> 82 gaggttgaag gaccagggcg tgtcagccct gtcacagaga ccttgggc atg gag gag
83 57
84
85 Met Glu Glu
1
E--> 87 agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc
88 105
89 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile
90 5 10 15
E--> 92 cca ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg
93 153
94 Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser Cys Ser Val
95 20 25 30 35
E--> 97 gcc cgg gtg ggt ctg ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg
98 201
99 Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly Ala Gly Leu
100 40 45 50
E--> 102 gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag
103 249
104 Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu
105 55 60 65
E--> 107 atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg
108 297
109 Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu
110 70 75 80
E--> 112 ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca
113 345
114 Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr
115 85 90 95
E--> 117 ggg gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag
118 393
119 Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu
120 100 105 110 115
E--> 122 act cag ctg ggc ctg gcc tcc ctg agg ggc ctc agc tac cac gat ggg
123 441
124 Thr Gln Leu Gly Leu Ala Ser Leu Arg Gly Leu Ser Tyr His Asp Gly
125 120 125 130

```

*same**same*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/549,096A

DATE: 02/19/2002

TIME: 12:16:00

Input Set : A:\Sequence Listing.asc

Output Set: N:\CRF3\02192002\I549096A.raw

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E--> 127 gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg
      128 489
      129 Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
      130                               135                               140                               145
E--> 132 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc
      133 537
      134 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
      135                               150                               155                               160
E--> 137 cac ggc ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg
      138 585
      139 His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu
      140                               165                               170                               175
E--> 142 ttg gtc agc cag cag tca ccc tgc gga cgg gcc acc agc agc tcc cgg
      143 633
      144 Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg
      145 180                               185                               190                               195
E--> 147 gtc tgg tgg gac agc agc ttc ctg ggt ggt gtg gta cac ctg gag gct
      148 681
      149 Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His Leu Glu Ala
      150                               200                               205                               210
E--> 152 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg
      153 729
      154 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
      155                               215                               220                               225
E--> 157 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga
      158 771
      159 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
      160                               230                               235                               240
E--> 162 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc
      163 831
E--> 165 aggggaaaga aaactcacga agcagaggct gggcgtggtg gctctcgcct gtaatcccag
      166 891
E--> 168 cactttggga ggccaaggca ggcggatcac ctgaggtcag gagttcgaga ccagcctggc
      169 951
E--> 171 taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tgggtggtgcc
      172 1011
E--> 174 tgcctgtaat ccagctactc aggaggctga ggcaggataa ttttgcttaa acccgggagg
      175 1071
E--> 177 cggagggttc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga
      178 1131
E--> 180 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
      181 1169

```

*same*



## VERIFICATION SUMMARY

DATE: 02/19/2002

PATENT APPLICATION: US/09/549,096A

TIME: 12:16:01

Input Set : A:\Sequence Listing.asc

Output Set: N:\CRF3\02192002\I549096A.raw

L:29 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:1  
L:42 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:2  
L:55 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:3  
L:68 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:4  
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:57 SEQ:5  
M:254 Repeated in SeqNo=5